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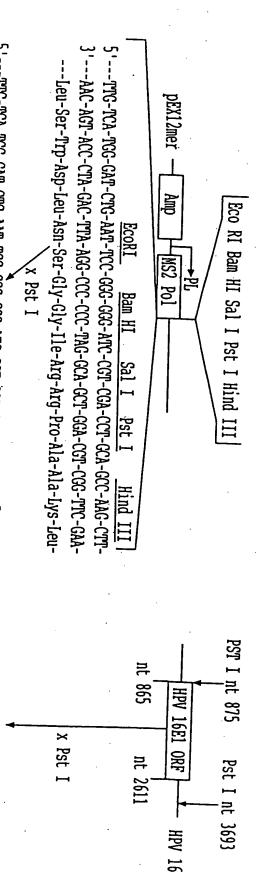
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5'---TTG-TCA-TGG-GAT-CTG-AAT-TCC-GGG-GGG-ATC-CGT-CGA-CCT-GCA-3'---AAC-AGT-ACC-CTA-GAC-TTA-AGG-CCC-CCC-TAG-GCA-GCT-GG ---Leu-Ser-Trp-Asp-Leu-Asn-Ser-Gly-Gly-Ile-Arg-Arg-Pro--Ala

5' -GGT-ACC-AAT-GGG-GAA-GAG-GGT-ACG-GGA-TGT-AAT--3' A-CGT-CCA-TGG-TTA-CCC-CTT-CTC-CCA-TGC-CCT-ACT-TTA---

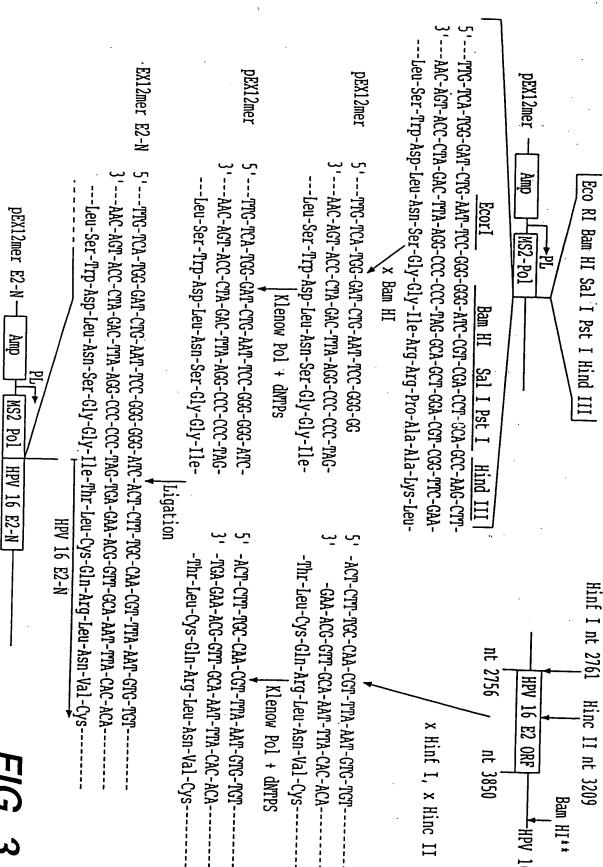
Ala-Gly-Thr-Asn-Gly-Glu-Glu-Gly-Thr-Gly-Cys-Asn---|Ligation

EX12merE1 5'----TTG-TCA-TGG-GAT-CTG-AAT-TCC-GGG-GGG-ATC-CGT-CGA-CCT-GCA-GGT-ACC-AAT-GGG-GAA-GAG-GGT-ACG-GGA-TGT-AAT---3'----AAC-AGT-ACC-CTA-GAC-TTA-AGG-CCC-CCC-TAG-GCA-GCT-GGA-CGT-CCA-TGG-TTA-CCC-CTT-CTC-CCA-TGC-CCT-ACA-TTA----Leu-Ser-Trp-Asp-Leu-Asn-Ser-Gly-Gly-Ile-Arg-Arg-Pro-Ala-Gly-Thr-Asn-Gly-Glu-Glu-Gly-Thr-Gly-Cys-Asn---pEX12merE1 Amp HPV 16 E1 HPV 16 E1

FIG. 1

CLONE	SEQUENCE	POSITION	ISOLATE
REGION	REGION E1-1090:		
1090	NGWFYVEAVVEKKTGDAISDDENENDSDTGEDLVDFIVNDNDYLT	As 16-60	-
1079	NENDSDTGEDLVDFIVND	AS 38-55	w
1084	MADPAGTINGEEGTGCNG\\TYVEAVVEKKTGDA I SDDENENDSDTGEDLVDF I VNDNDYLT	AS 1-60	w
1029	EDLVDFIVNDNDYLT	AS 46-60	5
1099	EDLVDFTVNDNDYLTQAETETAHALFTAQEAKQH	AS 46-79	5
1145	NENDSDTGEDLVDFT VNDNDYLTQAETETAHALFTAQEAKQHRDAVQVLKRKYLvvh	AS 38-91	-
REGION	REGION E1-1059:		
1059	stgsktkvfGSPLSDIS	AS 92-99	

FIG. 2



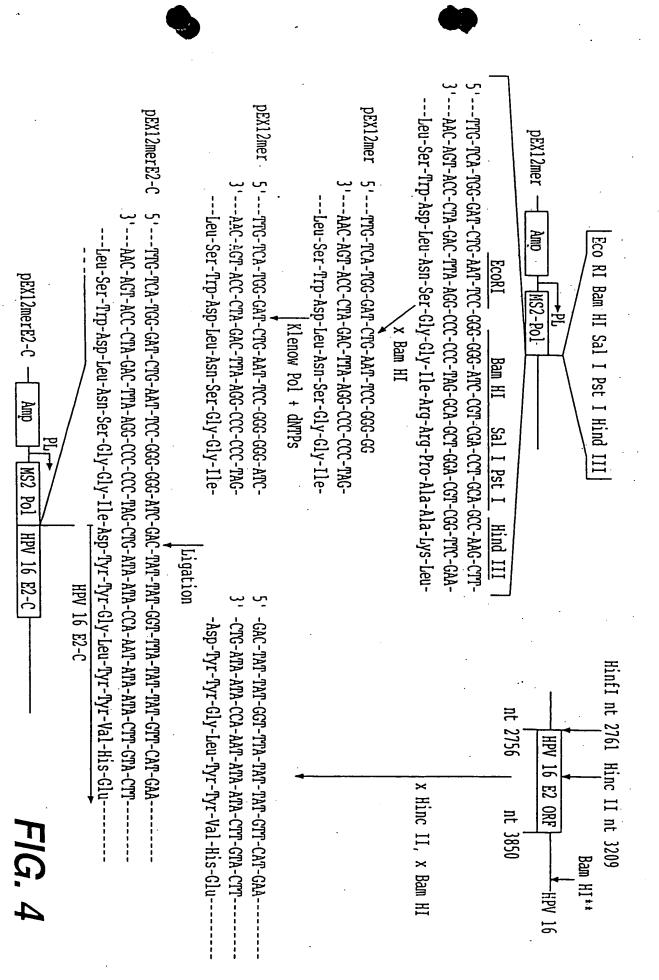


FIG. 5

~	AS 231-249	TEETQTTIQRPRSEPDICN	1091
	AS 209-245	EI IRQHLANHPAATHTKAVALGTEETQTTI QRPRSEP	REGION E2-1102: 1102
2	AS 199-234	VFSSNEVSSPEIIRQHLANHPAATHTKAVALGTEET	1121
	AS 197-211	TSVFSSNEVSSPEII	1158
			REGION E2-1158:
-	AS 78-91	TLETIYNSQYSNEK	1156
<u></u>	AS 76-100	QLTLETIYNSQYSNEKWTLQDVSLE	1112
			REGION E2-1112:
2	AS 61-76	TLAVSKNKALQATELQLTLETTYNSQYSNEKWTLQDV	1018
4	AS 55-70	INHQVVPTLAVSKNKAL	1057
-	AS 55-73	INHQVVPTLAVSKNKALQAI	1063
	AS 43-67	YYKAREMGFKHINHQVVPTLAVSKN	1061
2	AS 41-70	AIYYKARENGFKHINHQVVPTLAVSKNKAL	1060
4	AS 41-63	AIYYKARENGFKHINHQVVPTLA	1074
			REGION E2-1074:
2	AS 25-35	DLRDHIDYWKH	1170
			REGION E2-1170:
5	AS 13-30	DSTDLRDHI	1025 DKILTHYENDSTDLRDHI
<u>س</u>	AS 13-23	DS	1066 DKILTHYENDS
			REGION E2-1066:
ISOLATE	POSITION	SEQUENCE	CLONE